

TTGGGACCCGACAGGACACAGGAGGAGTCAAGTGCATCTCTGGGACCCGACAGGACAGGCTCCCGACCCGAGGCTCTCA

GAGGCCAGTCTCTTTTCCCTCCCAAGCCATCTTCAACCCAGGTGAGGACAGAGG	M L A G G V R	7
ATG CTG GCG GGG GGC GTG AGG		151
S M P S P L L A C W Q P I L L L V L G S		27
AGC ATG CCC AGC CCC CTC CTG GCG TGC TGG CAG CCC ATC CTC CTG CTG GTG CTG GGC TCA		211
V L S G S A T G C P P R C E C S A Q D R		47
CTG CTG TCA GCG TCG GCG ACG GCG TGC CCG CCC CCG TGC GAG TGC TCC GCG CAG GAC CCG		271
A V L C H R K R F V A V P E G I P T E T		67
GCT GTG CTG TGC CAC CCG AAG CCG TTT GTG GCA GTC CCC GAG GGC ATC CCC ACC GAG ACG		331
R L L D L G K N R I K T L N Q D E F A S		37
CGC CTG CTG GAC CTA GCG AAG AAC CCG ATC AAA ACG CTC AAC CAG GAC GAG TTC GCC AGC		391
F P H L E E L E L N E N I V S A V E P G		107
TTT CCG CAC CTG GAG GAG CTG GAG CTC AAC GAG AAC ATC GTG AGC CCC GTG GAG CCC GCG		451
A F N N L F N L R T L G L R S N R L K L		127
GCC TTC AAC AAC CTC TTC AAC CTC CCG ACG CTG GGT CTC CCG AGC AAC CCG CTG AAG CTC		511
I P L G V F T G L S N L T K L D T R E N		147
ATC CCG CTA GCG GTC TTC ACT GCG CTC AGC AAC CTG ACC AAG CTG GAC ACG AGG GAG AAC		571
K I V I L L D Y M F Q D L Y N L K S L E		167
AAG ATC GTT ATC CTA CTG GAC TAC ATG TTT CAG GAC CTG TAC AAC CTC AAG TCA CTG GAG		631
V G D N D L V Y I S H R A F S G L N S L		187
GTT GCG GAC AAT GAC CTC GTC TAC ATC TCT CAC CCG GCG TTC AGC GCG CTC AAC AGC CTG		691
E Q L T L E K C N L T S I P T E A L S H		207
GAG CAG CTG ACT CTG GAG AAA TGC AAC CTG ACC TCC ATC CCC ACC GAG GCG CTG TCC CAC		751
L H G L I V L R L R H L N I N A I R D Y		227
CTG CAC GCG CTC ATC GTC CTG AGG CTC CCG CAC CTC AAC ATC AAT GCG ATC CCG GAC TAC		311
S F K R L Y R L K V L E I S H W P Y L D		247
TCC TTC AAG AGG CTG TAC CGA CTC AAG GTC TTG GAG ATC TCC CAC TGG CCC TAC TTG GAC		371
T M T P N C L Y G L N L T S L S I T H C		267
ACC ATG ACA CCC AAC TGC CTC TAC GCG CTC AAC CTG ACG TCC CTG TCC ATC ACA CAC TCC		931
N L T A V P Y L A V R H L V Y L R F L N		287
AAT CTG ACC GGT GTG CCC TAC CTG GCG GTC CCG CAC CTA GTC TAT CTC CCG TTC CTC AAC		991
L S Y N P I S T I E G S M L H E L L R L		307
CTC TCC TAC AAC CCC ATC AGC ACC ATT GAG GCG TCC ATG TTG CAT GAG CTG CTC CCG CTG		1051
Q E I Q L V G G Q L A V V E P Y A F R G		327
CAG GAG ATC CAG CTG GTG GCG GCG CAG CTG GCG GTG GTG GAG CCC TAT GCG TTC CCG GCG		1111
L N Y L R V L N V S G N Q L T T L E E S		347
CTC AAC TAC CTG CCG GTG CTC AAT GTC TCT GCG AAC CAG CTG ACC ACA CTG GAG GAA TCA		1171

FIG. 1A

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V F H S V G N L E T L I L D S N P L A C	367
GTC TTC CAC TCG GTG GGC AAC CTG GAG ACA CTC ATC CTG GAC TCC AAC CCG CTG CCC TCC	1231
D C R L L W V F R R R W R L N F N R Q Q	387
CAC TGT CCG CTC CTG TGG GTG TTC CCG CGC CCC TGG CCG CTC AAC TTC AAC CCG CAG CAG	1291
P T C A T P E F V Q G K E F K D F P D V	407
CCC ACC TGC GCC ACC CCC GAG TTT CTC CAG GGC AAG GAG TTC AAG GAC TTC CCT GAT GTG	1351
L L P N Y F T C R R A R I R D R K A Q Q	427
CTA CTG CCC AAC TAC TTC ACC TGC CGC CGC GCC CGC ATC CCG GAC CGC AAG GCC CAG CAG	1411
V F V D E G H T V Q F V C R A D G D P P	447
GTG TTT GTG GAC GAG GGC CAC ACG GTG CAG TTT GTG TGC CCG GCC GAT GGC GAC CCG CCG	1471
P A I L W L S P R K H L V S A K S N G R	467
CCC GCC ATC CTC TGG CTC TCA CCC CGA AAG CAC CTG GTC TCA GCC AAG AGC AAT GGG CCG	1531
L T V F P D G T L E V R Y A Q V Q D N G	487
CTC ACA GTC TTC CCT GAT GGC ACG CTG GAG GTG CGC TAC GCC CAG GTA CAG GAC AAC GCC	1591
T Y L C I A A N A G G N D S M P A H L H	507
ACG TAC CTG TGC ATC CGC GCC AAC CGC GGC GGC AAC GAC TCC ATG CCC GCC CAC CTG CAT	1651
V R S Y S P D W P H Q P N K T F A F I S	527
GTG CCC ACG TAC TCG CCC GAC TGG CCC CAT CAG CCC AAC AAG ACC TTC GCT TTC ATC TCC	1711
N Q P G E G E A N S T R A T V P F P F D	547
AAC CAG CCG GGC GAG GGA GAG GCC AAC AGC ACC CGC GCC ACT GTG CCT TTC CCC TTC GAC	1771
I K T L I I A T T M G F I S F L G V V L	567
ATC AAG ACC CTC ATC ATC CCC ACC ACC ATG GGC TTC ATC TCT TTC CTG GGC GTC GTC CTC	1831
F C L V L L F L W S R G K G N T K H N I	587
TTC TGC CTG GTG CTG CTG TTT CTC TGG AGC CCG GGC AAG GGC AAC ACA AAG CAC AAC ATC	1891
E I E Y V P R K S D A G I S S A D A P R	607
GAG ATC GAG TAT GTG CCC CGA AAG TCG GAC CGA GGC ATC AGC TCC GCC GAC CGC CCC CGC	1951
K F N M K M I *	615
AAG TTC AAC ATG AAG ATG ATA TGA	1975
GGCCCCGGGGGGGGGGGAGGGACCCCCGGGGGGGGGGGGGACGGGAAGGGGGCCTGGCCGCCACCTGCTCACTCTCCAGTCC	2054
TTCCCACTCTCTCCCTACCCCTTCTACACAGTTCTCTTTCTCCCTCTCCGGCTCCCTTCCCTGCTGCCCCCGGCCAGCC	2133
CTCACCACTTGCCCTCTCTTCTACCAAGGACCTCAGAAGCCCCAGACCTGGGGACCCCACTACACAGGGGCATTGACAGAC	2212
TGGAGTTTAAGGGGACGAAACCGACACCGGGGAGAGTCAATAATTCAATAAAAAAGTTACGAACCTTTCTCTGTAAC TTG	2291
GGTTTCAATAAATTATGGATTTTTATGAAAACCTGAAATATAAAAAAAAAAAAAAAAAAAAAG	2351

FIG. 1B

		M A G S P											
3AATTCCGACGAGGCCAGCCAGTCCGCCSG/MCGRRGCCCGGCTCCCTGGGGCAGC	ATG GCG GGG TCG CCG	72											
L L W G P R A G G V G L L V L L L L G L	25												
CTG CTC TCG GCG CCG CCG GCC GCG GCG CTC GCG CTT TTG GTG CTG CTG CTG CTC GCG CTG	132												
F R P P P A L C A R P V K E P R G L S A	45												
TTT CCG CCG CCC CCC CCG CTC TGC GCG CCG CCG GTA AAG GAG CCC CCG GCG CTA AGC GCA	132												
A S P P L A E T G A P R R F R R S V P R	55												
GCG TCT CCG CCC TTG GGT GAG ACT GCG GCT CCG CCG CCG TTC CCG CCG TCA GTG CCC CGA	252												
G E A A G A V Q E L A R A L A H L L E A	85												
GGT GAG GCG GCG GCG GCG GTG CAG GAG CTG GCG CCG GCG CTG GCG CAT CTG CTG GAG GCG	312												
E R Q E R A R A E A Q E A E D Q Q A R V	105												
GAA CGT CAG GAG CCG CCG CCG GCG GAG GCG CAG GAG GCT GAG GAT CAG CAG GCG CCG GTC	372												
L A Q L L R V W G A P R N S D P A L G L	125												
CTG GCG CAG CTG CTG CCG CTC TCG GCG GCG CCG CCG AAC TCT GAT CCG GCT CTG GCG TTG	432												
D D D P D A P A A Q L A R A L L R A R L	145												
GAC GAC GAC CCC GAC CCG CCG GCA GCG CAG CTC GGT CCG GCT CTG CTC CCG CCG CCG CTT	492												
D P A A L A A Q L V P A P V P A A A L R	165												
GAC CCG GCG GCG CTA GCA GCG CAG CTT GTC CCC GCG CCG GTC CCC GCG GCG GCG CTC CGA	552												
P R P P V Y D D G P A G P D A E E A G D	185												
CCC CCG CCC CCG GTC TAC GAC GAC GCG CCC GCG GCG CCG GAT CCT GAG GAG GCA GCG GAC	612												
E T P D V D P E L L R Y L L G R I L A G	205												
GAG ACA CCC GAC GTG GAC CCC GAG CTG TTG AGG TAC TTG CTG GGA CCG ATT CTT GCG GGA	672												
S A D S E G V A A P R R L R R A A D H D	225												
AGC CCG GAC TCC GAG GCG GTG GCA GCG CCG CCG CCG CTC CCG CCG GCG GCG GAC CAC GAT	732												
V G S E L P P E G V L G A L L R V K R L	245												
GTG GCG TCT GAG CTG CCC CCG GAG GCG GTG CTG GCG GCG CTG CTG CCG GTG AAA CCG CTA	792												
E T P A P Q V P A R R L L P P *	261												
GAG ACC CCG GCG CCC CAG GTG CCG GCA CCG CCG CTC TTG CCA CCC TGA	840												
GCACCTCCCGGATCCCTGTCACCCCTGGGACCCAGAGTCCCCCGCCCATCCCGCCACACAGGACTGCTCCCCCGCCAGCAC	919												
GTCCAGAGCAACTTACCCCGGCCAGCCAGCCCTCTCAACCCAGGATCCCTACCCCGTCCG	979												

FIG. 2

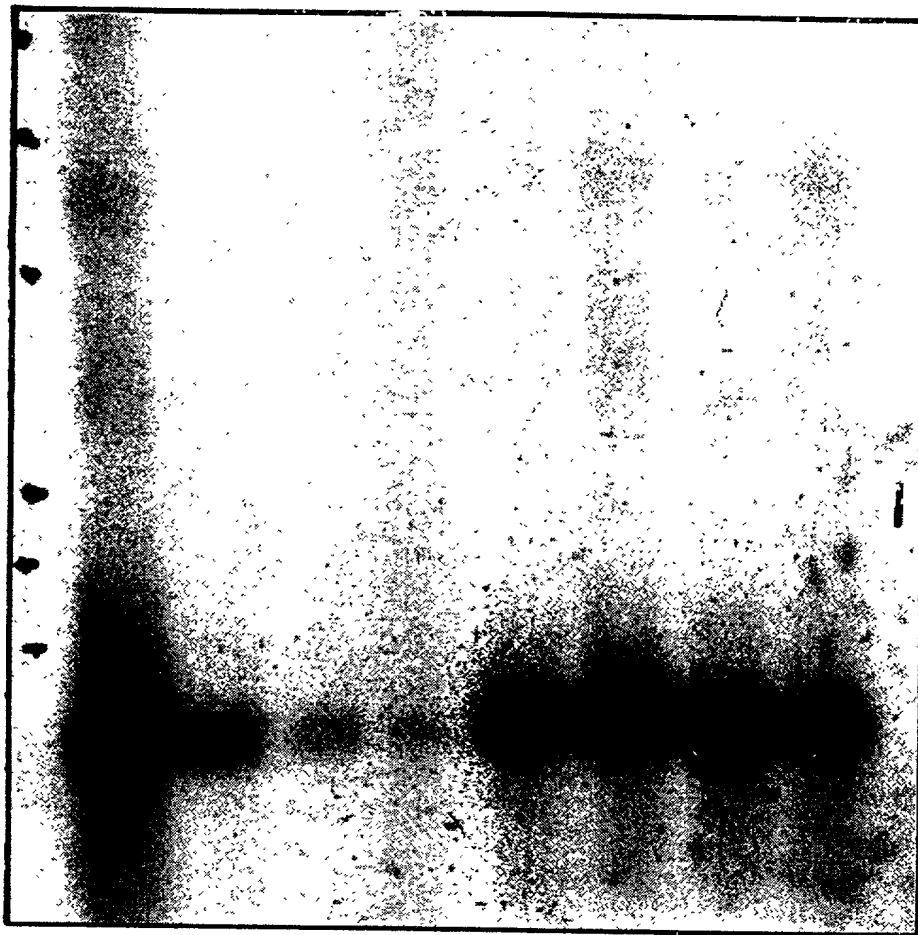
Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	1500	500	500	3000
Health status	0.8	0.2	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.7	0.3	0	1
Work satisfaction	0.6	0.5	0	1
Life satisfaction	0.7	0.4	0	1
Depression score	10.5	5.0	0	30
Anxiety score	12.0	6.0	0	30
Quality of life score	75.0	10.0	50	100

FIG. 3A

		: :: .	
D45913	566	PHITYTARVPVDVHEYNLHLQBSTDYEVCLTVSNIHQQTQKSCVNVTTK	615
T79	541	TVPPFDIKTLIIATTMGFI..SFLGVVLFCLVLLFLWSRGKGNTKHIE	588
		.: : : :~: : :~: : : : :~: . .. :	
D45913	616	TAAFALDISDHETSTALAAVMGSMFAVISLASIAIYIAKRFRKKNYHSL	665
T79	589	IEYVPRKSDAGISSADAPRKFNMMI.....	614
		. :~:~ . .~:~ . : :~.	
D45913	666	KKYMQKTSSIPLNEL.YPPLINLWEADSDKDKDGSADTKPTQVDTSRSYY	714

FIG. 3B

FIG. 4



205710" 683E0860

P D S T S V C V Q G Q C V K A G C D R I 399
 CCA GAT TCC ACC TCT GTC TGT GTG CAA GGA CAG TGT GTA AAA GCT GGT TGT GAT CCC ATC 1199

I D S K K K F D K C G V C G G N G S T C 419
 ATA GAC TCC AAA AAG AAG TTT GAT AAA TGT GGT GTT TCC GGG GGA AAT GGA TCT ACT TGT 1259

K K I S G S V T S A K P G Y H D I I T I 439
 AAA AAA ATA TCA GGA TCA GTT ACT AGT GCA AAA CCT GGA TAT CAT GAT ATC ATC ACA ATT 1319

P T G A T N I E V K Q R N Q R G S R N N 459
 CCA ACT GGA GCC ACC AAC ATC GAA GTG AAA CAG CGG AAC CAG AGG GGA TCC AGG AAC AAT 1379

G S F L A I K A A D G T Y I L N G D Y T 479
 GGC AGC TTT CTT GCC ATC AAA GCT GCT GAT GGC ACA TAT ATT CTT AAT GGT GAC TAC ACT 1439

L S T L E Q D I M Y K G V V L R Y S G S 499
 TTG TCC ACC TTA GAG CAA GAC ATT ATG TAC AAA GGT GTT GTC TTG AGG TAC AGC GGC TCC 1499

S A A L E R I R S F S P L K E P L T I Q 519
 TCT GCG GCA TTG GAA AGA ATT CGC AGC TTT AGC CCT CTC AAA GAG CCC TTG ACC ATC CAG 1559

V L T V G N A L R P K I K Y T Y F V K K 539
 GTT CTT ACT GTG GGC AAT GCC CTT CCA CCT AAA ATT AAA TAC ACC TAC TTC GTA AAG AAG 1619

K K E S F N A I P T F S A W V I E E W G 559
 AAG AAG GAA TCT TTC AAT GCT ATC CCC ACT TTT TCA GCA TGG GTC ATT GAA GAG TGG GGC 1679

E C S K T C G K G Y K K R S L K C L S H 579
 GAA TGT TCT AAG ACC TGT GGG AAG GGT TAC AAA AAA AGA AGC TTG AAG TGT CTG TCC CAT 1739

D G G V L S H E S C D P L K K P K H F I 599
 GAT GGA GGG GTG TTA TCT CAT GAG AGC TGT GAT CCT TTA AAG AAA CCT AAA CAT TTC ATA 1799

D F C T M A E C S * 609
 GAC TTT TGC ACA ATG GCA GAA TGC AGT TAA 1829

GTGGTTTAAGTGGTGTAGCTCTCAGGGCAAGGCCAAAGTGAAGGAAGGGCTGGTCCAGGGGAAGCAAGAAGGCTGGAGGG 1908

ATCCAGGGTATCTTCCAGTAACCACTGAGGTGTATCAGTAAGGTGGGATTAAGGGGTAGATAGAAAAGGAGTTGAAT 1987

CATCAGAGTAAGTCCAGTTGCCAATTTGATAGGATAGTTAGTGAAGGATTATTACCTCTGAGCAGTGATATAGCATA 2066

ATAAAGCCCCGGGCATTATTATTATTATTCTTTTGTACATCTATTACAAGTTTAGAAAAACAAGCAATTGTCAA 2145

AAAAGTGAAGTATTACAACCCCTGTTTCCCTGGTACTTATCAAATACTTAGTATCATGGGGGTGGGAATGAAAAGT 2224

AGGAGAAAGTGAGATTTTACTAAGACCTGTTTACTTTACCTCACTAACAATGGGGGGGAAGGAGTACAAATAGGA 2303

TCTTTGACGACGCTGTTTATGGCTGCTATGGTTTCAGAGAATGTTTATACATTATTTCACCGAGAATTAAGCTTCA 2382

GATTGTTCAACATGAGAGAAAGGCTCGCAACCTGAAATAACGCCAAATGGCTTCCCTCTTCTTTTGGACCATCTCA 2461

GTCTTTATTGTGTAAATTCATTTTCAGGAAAAACAACCTCCATGTATTTATTCAAGTGCATTAAAGTGTACAATGGAAA 2540

AAAAGCAGTGAAGCATTAGATGCTGGTAAAGCTAGAGGAGACACAATGAGCTTAGTACCTCCACTTCCCTTTCTTCC 2619

TACCATGTAAACCTGCTTTGGGAATATGGATGTAAAGAAGTAACTTGTGTCTCATGAAAATCAGTACATCACACAAGG 2698

FIG. 5B

AGGATGAAACGCCCCAACAATAAGAGGTGTCTAGAACAGGCTCCCAAGGTTTGGGGACATTGAGATCAGTTTCTTC	2777
TGGTGGGGAGGGTCTCTGAGGGTAACAGGTCCTCTCTGCGAGCTGGTCCAAAGTCCGTAACCTGGTGAATGTCTCTTC	2856
AGCTCTCTCTCTGAGAAATATGATTTTTTCCCTATGTTATATAGTAAAAATATGTTACTATTAATTACATGTACTTTTATAGT	2935
ATTGGTTTGGGTCTCTCTTCCAAAGAGGACTATAGTTAGTAAATAAATGCCCTATAATAACATATTTATTTTATACATTT	3014
ATTCTAATGAAAAAACTTTTAAATTATATCCCTTTTGGAACTGCATATAAATAGAGTATTTATACATATATGT	3093
TACTAGAAATAAAAGAACCTTTTGGAAAAAAGGGGGGGGGC	3147

FIG. 5C

251 DQSMADFHSGSLKHVLLTLFSVAARFYKHPSIRNSISLVVVKILVYEEQ 300
 1TRPILVDEEQ 11
 301 KGPEVTSNAALTTLRNFCNWKQHNSPSDRDFEHYDTAILFTQDLCGSH 350
 12 KGPEVTSNAALTTLRNFCNWKQHNSPSDRDAEHYDTAILFTQDLCGSQT 61
 351 CDTLGMADVGVTCDFSRSCSVIEDDGLQAFTTAHELGHVFNMPHDDAKH 400
 62 CDTLGMADVGVTCDFSRSCSVIEDDGLQAFTTAHELGHVFNMPHDDAKQ 111
 401 CASLNGVSGDSHLMASMLSSLCHSQFWSPCSAYMYTSFLDNHGGECLMDK 450
 112 CASLNGVNGDSHLMASMLSNLCHSQFWSPCSAYMYTSFLDNHGGECLMDK 161
 451 PQNPILKPSDLPGTLVDANRQCQFTTGEESKHCPODAASTCTILNCTGTSG 500
 162 PQNPILKPSDLPGTLVDANRQCQFTTGEDSKHCPODAASTCTILNCTGTSG 211
 501 GLLVCQTHXFPWADGTSCGEGKWCVSGKVCNCTDMKHFATPVHGSNGPWG 550
 212 GVLVCQTHXFPWADGTSCGEGKWCINGKVCNCTDMKHFATPVHGSNGPWG 261
 551 FWGDCSRTCCGGVQYTMRECNFVPFNGGKYCEGKRVYRSCNLEDPCPN 600
 262 FWGDCSRTCCGGVQYTMRECNFVPFNGGKYCEGKRVYRSCNLEDPCPN 311
 601 NGKTFREEQCEAHNEFSKASFGNEPTVWTPKAGVSPKDRCKLTCEAKG 650
 312 NGKTFREEQCEAHNEFSKASFGSGPAVENTPKAGVSPKDRCKLTCEAKG 361
 651 IGYFFVLQPKVVDGTPCSFSDTSVVCVQGCVKAGCDRIIDSKKKPFKQGV 700
 362 IGYFFVLQPKVVDGTPCSFSDTSVVCVQGCVKAGCDRIIDSKKKPFKQGV 411
 701 CGGNGSTCKKMSGIVTSTRPGYHDIIVTIPAGATNIEVKHFNQGRSFRNGS 750
 412 CGGNGSTCKKLSGVTSAKPGYHDIITITPTGATNIEVKHFNQGRSFRNGS 461
 751 FLAIRAADGTYILNGFTLSTLEQDLTYKGTVLRYSGSSAALERIRSFSP 800
 462 FLAIRAADGTYILNGFTLSTLEQDLTYKGTVLRYSGSSAALERIRSFSP 511
 801 LKEPLTIQVLTVGNALRPKIDTYFMQKTESFNAIPTFSEWVIEEWEC 850
 512 LKEPLTIQVLTVGNALRPKIDTYFMQKTESFNAIPTFSAWVIEEWEC 560
 901 WSPCKSKTCKGKYKGRSLKCVSHDGGVLSNESCDPLKKPKHFIDFCILTQC 950
 561 ...CSKTCKGKYKGRSLKCLSHDGGVLSHESCDPLKKPKHFIDFCILTQC 607
 951 S* 951
 608 S* 609

FIG. 6

FIG. 6

gtgcctac atg gtc acg tcc ttc cta gat aat gga cac ggg gaa tgt ttg	50
Met Val Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu	
1 5 10	
atg gac aag ccc cag aat cca atc aag ctc cct tct gat ctt ccc ggt	98
Met Asp Lys Pro Gln Asn Pro Ile Lys Leu Pro Ser Asp Leu Pro Gly	
15 20 25 30	
acc ttg tac gat gcc aac cgc cag tgt cag ttt aca ttc gga gag gaa	146
Thr Leu Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Glu	
35 40 45	
tcc aag cac tgc cct gat gca gcc agc aca tgt act acc ctg tgg tgc	194
Ser Lys His Cys Pro Asp Ala Ala Ser Thr Cys Thr Thr Leu Trp Cys	
50 55 60	
act ggc acc tcc ggt ggc tta ctg gtg tgc caa aca aaa cac ttc cct	242
Thr Gly Thr Ser Gly Gly Leu Leu Val Cys Gln Thr Lys His Phe Pro	
65 70 75	
tgg gca gat ggc acc agc tgt gga gaa ggg aag tgg tgt gtc agt ggc	290
Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Val Ser Gly	
80 85 90	
aag tgc gtg aac aag aca gac atg aag cat ttt gct act cct gtt cat	338
Lys Cys Val Asn Lys Thr Asp Met Lys His Phe Ala Thr Pro Val His	
95 100 105 110	
gga agc tgg gga cca tgg gga ccg tgg gga gac tgc tca aga acc tgt	386
Gly Ser Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys	
115 120 125	
ggt ggt gga gtt caa tac aca atg aga gaa tgt gac aac cca gtc cca	434
Gly Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro	
130 135 140	
aag aac gga ggg aag tac tgt gaa ggc aaa cga gtc cgc tac agg tcc	482
Lys Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser	
145 150 155	
tgt aac atc gag gac tgt cca gac aat aac gga aaa acg ttc aga gag	530
Cys Asn Ile Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu	
160 165 170	
gag cag tgc gag gcg cac aat gag ttt tcc aaa gct tcc ttt ggg aat	578
Glu Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Asn	
175 180 185 190	
gag ccc act gta gag tgg aca ccc aag tac gcc ggc gtc tcg cca aag	626
Glu Pro Thr Val Glu Trp Thr Pro Lys Tyr Ala Gly Val Ser Pro Lys	
195 200 205	

FIG. 7A

gac agg tgc aag ctc acc tgt gaa gcc aaa ggc att ggc tac ttt ttc	674
Asp Arg Cys Lys Leu Thr Cys Glu Ala Lys Gly Ile Gly Tyr Phe Phe	
210 215 220	
gtc tta cag ccc aag gtt gta gat ggc act ccc tgt agt cca gac tct	722
Val Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser	
225 230 235	
acc tct gtc tgt gtg caa ggg cag tgt gtg aaa gct ggc tgt gat cgc	770
Thr Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg	
240 245 250	
atc ata gac tcc aaa aag aag ttt gat aag tgt ggc gtt tgt gga gga	818
Ile Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly	
255 260 265 270	
aac ggt tcc aca tgc aag aag atg tca gga ata gtc act agt aca aga	866
Asn Gly Ser Thr Cys Lys Lys Met Ser Gly Ile Val Thr Ser Thr Arg	
275 280 285	
cct ggg tat cat gac att gtc aca att cct gct gga gcc acc aac att	914
Pro Gly Tyr His Asp Ile Val Thr Ile Pro Ala Gly Ala Thr Asn Ile	
290 295 300	
gaa gtg aaa cat cgg aat caa agg ggg tcc aga aac aat ggc agc ttt	962
Glu Val Lys His Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe	
305 310 315	
ctg gct att aga gcc gct gat ggt acc tat att ctg aat gga aac ttc	1010
Leu Ala Ile Arg Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asn Phe	
320 325 330	
act ctg tcc aca cta gag caa gac ctc acc tac aaa ggt act gtc tta	1058
Thr Leu Ser Thr Leu Glu Gln Asp Leu Thr Tyr Lys Gly Thr Val Leu	
335 340 345 350	
agg tac agt ggt tcc tcg gct gcg ctg gaa aga atc cgc agc ttt agt	1106
Arg Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser	
355 360 365	
cca ctc aaa gaa ccc tta acc atc cag gtt ctt atg gta ggc cat gct	1154
Pro Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Met Val Gly His Ala	
370 375 380	
ctc cga ccc aaa att aaa ttc acc tac ttt atg aag aag aag aca gag	1202
Leu Arg Pro Lys Ile Lys Phe Thr Tyr Phe Met Lys Lys Lys Thr Glu	
385 390 395	
tca ttc aac gcc att ccc aca ttt tct gag tgg gtg att gaa gag tgg	1250
Ser Phe Asn Ala Ile Pro Thr Phe Ser Glu Trp Val Ile Glu Glu Trp	
400 405 410	

FIG. 7B

ggg gag tgc tcc aag aca tgc ggc tca ggt tgg cag aga aga gta gtg 1298
Gly Glu Cys Ser Lys Thr Cys Gly Ser Gly Trp Gln Arg Arg Val Val
115 420 425 430

cag tgc aga gac att aac gga cac cct gct tcc gaa tgt gca aag gaa 1346
Gln Cys Arg Asp Ile Asn Gly His Pro Ala Ser Glu Cys Ala Lys Glu
435 440 445

gtg aag cca gcc agt acc aga cct tgt gca gac ctt cct tgc cca cac 1394
Val Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp Leu Pro Cys Pro His
450 455 460

tgg cag gtg ggg gat tgg tca cca tgt tcc aaa act tgc ggg aag ggt 1442
Trp Gln Val Gly Asp Trp Ser Pro Cys Ser Lys Thr Cys Gly Lys Gly
465 470 475

tac aag aag aga acc ttg aaa tgt gtg tcc cac gat ggg ggc gtg tta 1490
Tyr Lys Lys Arg Thr Leu Lys Cys Val Ser His Asp Gly Gly Val Leu
480 485 490

tca aat gag agc tgt gat cct ttg aag aag cca aag cat tac att gac 1538
Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp
495 500 505 510

ttt tgc aca ctg aca cag tgc agt taagaggcgt tagaggacaa ggtagcgtgg 1592
Phe Cys Thr Leu Thr Gln Cys Ser
515

ggaggggctg atacactgag tgcaagagta ctggagggat ccagtgagtc aaaccagtaa 1652
gcagtgaggt gtggcaagga ggtgtgtgta ggggatacat agcaaaggag gtagatcagg 1712
acaactacct gccagttaca ttctgataag gtagttaatg aggcacagta gcatctgaaa 1772
gaccatacag agcactaagg agcccaaaag cactattagt atctcttttc ttatatctat 1832
cgcccaaata attttcagag tctggcagaa gccctgttgc actgtactaa ctagatactt 1892
cttatcacia agattgggaa aggcaaagca gaaagatggt aagactgggt ttcaaaacag 1952
gcttggtttc aatcactgga ggcaaggagg aggggacaaa caagatcatt attcgaagtc 2012
gctgggttgc gtggttttac ggaagggtga tgcattcatc ctatcaacag tgaaaagttc 2072
agcttggtca acgtgacaga aaggctcatc tccgtgaaag agctcctgat ttcttcttac 2132
accatctcag ttcttaacta tagttcatgt tgaggtagaa acaattcatc tatttataaa 2192
atgtacattg gaaaaaaaaa gtgaagttta tgaggtagac ataaaaactg aaggaaacaa 2252
tgagcaacat gcctcctgct ttgcttctc ctgaggtaaa cctgcctggg gattgaggtt 2312
gtttaagatt atccatggct cacaagaggc agtaaaataa tacatgttgt gccagagtta 2372
gaatggggta tagagatcag ggtcccatga gatggggaac atgggtgatca ctcatctcac 2432
atgggaggct gctgcagggt agcaggcca ctcctggcag ctgggtccaac agtcgtatcc 2492
tggtgaatgt ctgttcagct cttctactga gagagaatat gactgtttcc atatgtatat 2552
gtatatagta aaatatgtta ctatgaattg catgtacttt ataagtattg gtgtgtctgt 2612
tccttctaag aaggactata gtttataata aatgcctata ataacatatt tatttttata 2672
catttatctc taatgataaa acccttaagt tatatcgctt ttgtaaaagt gcatataaaa 2732
atagagtatt tatacaatat atgttaacta gaaataataa aagaacactt ttgaatgtgt 2792
atgcctatct tctggagtgg gattaacttc tgggcaagaa atctgatgag acacaaacat 2852
tggacttcaa gacagtttta aattttgggt aaatgaactg tatttcctgt ttatagacgt 2912
actaataaaa aagaagttga tgatgtcttt agtggtaaga ttgttactaa tgtggttggc 2972
aaattgctgt aaagagccag atagtaagca tttatggcat tgtaggctat ctttctgccc 3032
acaaccatgt gacagtgagt gctttgtagg actgagagca gccataaatg acatgtaaat 3092
gataaactgt ggctgtgctt taataaaaact ttatttacaa aaaaaaaaaa aaa 3145

FIG. 7C

gagggcgctc ccggccgggc caagggacag agccaggctc cgggagcccg caacactcgt	60
cctgagagcc ccggctcctc agcccgtac ggccagggcc tgggctccg cccccgactc	120
ccgagctcct gccctagagt cgactygggt cccgcccgcg tgggacagac agacggacag	180
ccagccctgc gagggcgcg gcaccggggc gaggtgttgt aggaggagac cgaggagggg	240
ggctgggctg gggctggggc cgcgccggca agagagacat gcgattggtg accaagccga	300
gcggacggac agcgcgcccg ag atg cag gtg agc gag agg atg ctg gca ggg	352
Met Gln Val Ser Glu Arg Met Leu Ala Gly	
1 5 10	
ggt atg aga agc atg ccc agc ccc ctc ctg gcc tgc tgg cag ccc atc	400
Gly Met Arg Ser Met Pro Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile	
15 20 25	
ctc ctg ctg gta ctg ggc tca gtg ctg tca ggc tct gct aca ggc tgc	448
Leu Leu Leu Val Leu Gly Ser Val Leu Ser Gly Ser Ala Thr Gly Cys	
30 35 40	
ccg ccc cgc tgc gag tgc tca gcg cag gac cga gcc gtg ctc tgc cac	496
Pro Pro Arg Cys Glu Cys Ser Ala Gln Asp Arg Ala Val Leu Cys His	
45 50 55	
cgc aaa cgc ttt gtg gcg gtg ccc gag ggc atc ccc acc gag act cgc	544
Arg Lys Arg Phe Val Ala Val Pro Glu Gly Ile Pro Thr Glu Thr Arg	
60 65 70	
ctg ctg gac ctg ggc aaa aac cgc atc aag aca ctc aac cag gac gag	592
Leu Leu Asp Leu Gly Lys Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu	
75 80 85 90	
ttt gcc agc ttc cca cac ctg gag gag cta gaa ctc aat gaa aac atc	640
Phe Ala Ser Phe Pro His Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile	
95 100 105	
gtg agc gcc gtg gag cca ggc gcc ttc aac aac ctc ttc aac ctg agg	688
Val Ser Ala Val Glu Pro Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg	
110 115 120	
act ctg ggg ctg cgc agc aac cgc ctg aag ctt atc ccg ctg ggc gtc	736
Thr Leu Gly Leu Arg Ser Asn Arg Leu Lys Leu Ile Pro Leu Gly Val	
125 130 135	
ttc acc ggc ctc agc aac ttg acc aag ctg gac atc agt gag aac aag	784
Phe Thr Gly Leu Ser Asn Leu Thr Lys Leu Asp Ile Ser Glu Asn Lys	
140 145 150	
atc gtc atc ctg cta gac tac atg ttc caa gac cta tac aac ctc aag	832
Ile Val Ile Leu Leu Asp Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys	
155 160 165 170	
tgc ctg gag gtc ggc gac aac gac ctc gtc tac atc tcc cat cga gcc	880
Ser Leu Glu Val Gly Asp Asn Asp Leu Val Tyr Ile Ser His Arg Ala	
175 180 185	

FIG. 8A

Met Ala Gly Ser

atcctcaccg gaagttcggg gccagaggct gctcctgcc cgcgcgcct ccgccgatct 710
gtggaccagg atttgggtcc cgaggtgccc cctgagaacg tactgggggc tctgctacgc 770
gtcaaacgcc tggagaaccc ctgcgccag gcgccggcac qccqccctct qcctccctga 830

FIG. 9A

gcgctgctgc atcctgcacg ccctggaacc caggagcgcc ccagcaaccc tgactccctg 890
 ccagcacgtc caaggctgct tccccagca acctcccatc ccctgagccc tcaataaatg 950
 ccctctgtag caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1010
 aaaaaaaaaa aaaaaaa 1027

FIG. 9B

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